

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

Met	Ala	Ala	Val	Glu	Leu	Glu	Trp	Ile	Pro	Glu	Thr	Leu	Tyr	Asn	Thr
1				5					10					15	
Ala	Ile	Ser	Ala	Val	Val	Asp	Asn	Tyr	Ile	Arg	Ser	Arg	Arg	Asp	Ile
		20					25						30		
Arg	Ser	Leu	Pro	Glu	Asn	Ile	Gln	Phe	Asp	Val	Tyr	Tyr	Lys	Leu	Tyr
		35					40					45			
Gln	Gln	Gly	Arg	Leu	Cys	Gln	Leu	Gly	Ser	Glu	Phe	Cys	Glu	Leu	Glu
	50					55					60				
Val	Phe	Ala	Lys	Val	Leu	Arg	Ala	Leu	Asp	Lys	Arg	His	Leu	Leu	His
65					70					75				80	
His	Cys	Phe	Gln	Ala	Leu	Met	Asp	His	Gly	Val	Lys	Val	Ala	Ser	Val
			85						90					95	
Leu	Ala	Tyr	Ser	Phe	Ser	Arg	Arg	Cys	Ser	Tyr	Ile	Ala	Glu	Ser	Asp
			100					105						110	
Ala	Ala	Val	Lys	Glu	Lys	Ala	Ile	Gln	Val	Gly	Phe	Val	Leu	Gly	Gly
		115					120						125		
Phe	Leu	Ser	Asp	Ala	Gly	Trp	Tyr	Ser	Asp	Ala	Glu	Lys	Val	Phe	Leu
	130					135					140				
Ser	Cys	Leu	Gln	Leu	Cys	Thr	Leu	His	Asp	Glu	Met	Leu	His	Trp	Phe
145					150					155					160
Arg	Ala	Val	Glu	Cys	Cys	Val	Arg	Leu	Leu	His	Val	Arg	Asn	Gly	Asn
				165					170					175	
Cys	Lys	Tyr	His	Leu	Gly	Glu	Glu	Thr	Phe	Lys	Leu	Ala	Gln	Thr	Tyr
			180					185					190		
Met	Asp	Lys	Leu	Ser	Lys	His	Gly	Gln	Gln	Ala	Asn	Lys	Ala	Ala	Leu
		195					200						205		
Tyr	Gly	Glu	Leu	Cys	Ala	Leu	Leu	Phe	Ala	Lys	Ser	His	Tyr	Asp	Glu
	210					215						220			

Ala Tyr Lys Trp Cys Ile Glu Ala Met Lys Glu Ile Thr Ala Gly Leu
 225 230 235 240
 Pro Val Lys Val Val Val Asp Val Leu Arg Gln Ala Ser Lys Ala Cys
 245 250 255
 Val Val Lys Arg Glu Phe Lys Lys Ala Glu Gln Leu Ile Lys His Ala
 260 265 270
 Val Tyr Leu Ala Arg Asp His Phe Gly Ser Lys His Pro Lys Tyr Ser
 275 280 285
 Asp Thr Leu Leu Asp Tyr Gly Phe Tyr Leu Leu Asn Val Asp Asn Ile
 290 295 300
 Cys Gln Ser Val Ala Ile Tyr Gln Ala Ala Leu Asp Ile Arg Gln Ser
 305 310 315 320
 Val Phe Gly Gly Lys Asn Ile His Val Ala Thr Ala His Glu Asp Leu
 325 330 335
 Ala Tyr Ser Ser Tyr Val His Gln Tyr Ser Ser Gly Lys Phe Asp Asn
 340 345 350
 Ala Leu Phe His Ala Glu Arg Ala Ile Gly Ile Ile Thr His Ile Leu
 355 360 365
 Pro Glu Asp His Leu Leu Leu Ala Ser Ser Lys Arg Val Lys Ala Leu
 370 375 380
 Ile Leu Glu Glu Ile Ala Ile Asp Cys His Asn Lys Glu Thr Glu Gln
 385 390 395 400
 Arg Leu Leu Gln Glu Ala His Asp Leu His Leu Ser Ser Leu Gln Leu
 405 410 415
 Ala Lys Lys Ala Phe Gly Glu Phe Asn Val Gln Thr Ala Lys His Tyr
 420 425 430
 Gly Asn Leu Gly Arg Leu Tyr Gln Ser Met Arg Lys Phe Lys Glu Ala
 435 440 445
 Glu Glu Met His Ile Lys Ala Ile Gln Ile Lys Glu Gln Leu Leu Gly
 450 455 460
 Gln Glu Asp Tyr Glu Val Ala Leu Ser Val Gly His Leu Ala Ser Leu
 465 470 475 480
 Tyr Asn Tyr Asp Met Asn Gln Tyr Glu Asn Ala Glu Lys Leu Tyr Leu
 485 490 495
 Arg Ser Ile Ala Ile Gly Lys Lys Leu Phe Gly Glu Gly Tyr Ser Gly
 500 505 510
 Leu Glu Tyr Asp Tyr Arg Gly Leu Ile Lys Leu Tyr Asn Ser Ile Gly
 515 520 525
 Asn Tyr Glu Lys Val Phe Glu Tyr His Asn Val Leu Ser Asn Trp Asn
 530 535 540
 Arg Leu Arg Asp Arg Gln Tyr Ser Val Thr Asp Ala Leu Glu Asp Val
 545 550 555 560
 Ser Thr Ser Pro Gln Ser Thr Glu Glu Val Val Gln Ser Phe Leu Ile
 565 570 575
 Ser Gln Asn Val Glu Gly Pro Ser Cys
 580 585

<210> 2

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2

atggcggccg	tggaactaga	gtggatccca	gagactctct	ataacaccgc	catctccgct	60
gtcgtggaca	actacatccg	ctcccgccga	gacatccgct	ccttgcccga	gaacatccag	120
tttgatgttt	actacaagct	ttaccaacag	ggacgcttat	gtcaactggg	cagtgaattt	180
tgtgaattgg	aagtttttgc	taaagtactg	agagcttttg	ataaaagaca	tttgcttcac	240

```

cattgttttc aggctttgat ggatcatggg gttaaagttg cttcagtcctt ggcctactca      300
ttcagtaggc ggtgctctta tatagcagaa tcagatgctg cagtaaagga aaaagccatt      360
cagggttggt ttgttttagg tggctttctt tcagatgcag gctggtacag tgatgctgag      420
aaagtttttc tgtcctgcct tcagttgtgt actctacacg atgagatgct tcattgggtt      480
cgtgcagtag aatgttgtgt gaggttgctt catgtgcgaa atggaaaactg caaatatcat      540
ttgggtgaag aaacatttaa attagctcag acatatatgg ataaactatc aaaacatggc      600
cagcaagcaa ataaagctgc actctatgga gaactgtgtg cactcctatt tgcaaaaagt      660
cactatgatg aggcatacaa atggtgcatc gaggcaatga aagaaattac agcaggctta      720
ccagtgaag ttgtggtgga tgtcttaaga caagcttcta aggcttggtg agtaaaacgt      780
gaatttaaga aggcagaaca gttaattaaa catgcagtgt atttggcacg ggatcatttt      840
ggatccaaac acccaaaata ttctgataca ctgctagatt atgggttcta cttactcaat      900
gtagataata tctgtcagtc tgttgcaatt tatcaggcag cccttgacat tagacagtca      960
gtgtttgggt gcaaaaaatat ccacgtagca acagctcatg aagatttggc ctactcttct    1020
tatgtccacc agtatagctc tgggaaattt gacaatgcac tatttcatgc agaaagagct    1080
attggtatca ttaccacat cctacctgaa gatcatcttc ttttggcttc ttcaaagagg    1140
gtgaaagcac ttattttaga ggagattgca attgattgtc ataataagga aactgaacag    1200
aggctgcttc aagaagctca tgatttgcac ctgtcttcac tccaactagc taaaaaagct    1260
tttggggaat ttaatgtaca gactgcaaaa cactatggaa accttgggaag actttatcag    1320
tcaatgagaa aatttaagga agctgaagaa atgcacatca aagcaattca gattaaagaa    1380
caacttcttg gtcaagaaga ttatgaagta gccctttcag tgggacatct ggcttcttta    1440
tataattatg acatgaatca gtatgaaaaa gctgagaaac tttatttgcg atctatagca    1500
attgggaaga aacttttttg tgagggctac agtgactag aatatgatta tcgagggtctc    1560
attaaacttt acaactccat tggaaaattac gagaaagtgt ttgaatatca caatgttctg    1620
tctaactgga accggttgcg agatcggcaa tattcagtga cagatgctct tgaagatgtc    1680
agcaccagcc ccagtcacac tgaagaagtg gtgcagtcct tcctgatttc tcagaatgtc    1740
gagggaccga gctgctga                                     1758

```

<210> 3

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

```

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1              5              10              15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
      20              25              30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
      35              40              45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
      50              55              60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
      65              70              75              80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
      85              90              95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
      100             105             110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
      115             120             125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
      130             135             140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
      145             150             155             160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
      165             170             175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
      180             185             190

```

4

Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
 900 905 910
 Pro Ile Tyr Phe His Thr Gln
 915

<210> 4

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 4

cgagatcccg	gggagccagc	ttgctgggag	agcgggacgg	tccggagcaa	gcccacaggc	60
agaggaggcg	acagagggaa	aaagggccga	gctagccgct	ccagtgcgtg	acaggagccg	120
aagggacgca	ccacgccagc	cccagcccgg	ctccagcgac	agccaacgcc	tottgcagcg	180
cggcgggcttc	gaagccgccg	cccggagctg	ccctttcctc	ttcgggtgaag	tttttaaaag	240
ctgctaaaga	ctcggaggaa	gcaaggaaaag	tgccctggtag	gactgacggc	tgccctttgtc	300
ctcctcctct	ccaccccggc	tccccccacc	ctgccttccc	cccctcccc	gtcttctctc	360
ccgcagctgc	ctcagtcggc	tactctcagc	caacccccct	caccaccctt	ctccccaccc	420
gcccccccg	ccccgtcggc	ccagcgctgc	cagcccaggt	ttgcagagag	gtaactccct	480
ttggctgcga	gcgggagcgc	tagctgcaca	ttgcaaagaa	ggctcttagg	agccaggcga	540
ctggggagcg	gcttcagcac	tgacgcccag	accgcctgg	ttagaattcc	ggcggagaga	600
accctctgtt	ttccccact	ctctctccac	ctcctcctgc	cttccccacc	ccgagtgcgg	660
agcagagatc	aaaagatgaa	aaggcagtc	ggtcttcagt	agccaaaaaa	caaaaacaaac	720
aaaaacaaaa	aagccgaaat	aaaagaaaaa	gataataact	cagttcttat	ttgcacctac	780
ttcagtgagc	actgaatttg	gaaggtggag	gattttgttt	ttttctttta	agatctgggc	840
atcttttgaa	tctacccttc	aagtatttaag	agacagactg	tgagcctagc	agggcagatc	900
ttgtccaccg	tgtgtcttct	tctgcacgag	actttgaggg	tgtcagagcg	ctttttgcgt	960
ggttgctccc	gcaagtttcc	ttctctggag	cttcccgcag	gtgggcagct	agctgcagcg	1020
actaccgcat	catcacagcc	tgttgaactc	ttctgagcaa	gagaagggga	ggcggggtaa	1080

gggaagtagg	tggaagattc	agccaagctc	aaggatggaa	gtgcagttag	ggctgggaag	1140
ggtctaccct	cggccgccgt	ccaagaccta	cggaggagct	ttccagaatc	tgttccagag	1200
cgtgcgcgaa	gtgatccaga	acccggggcc	caggcaccga	gaggccgcga	gcgcagcacc	1260
tcccggcgcc	agtttgctgc	tgctgcagca	gcagcagcag	cagcagcagc	agcagcagca	1320
gcagcagcag	cagcagcagc	agcagcaaga	gactagcccc	aggcagcagc	agcagcagca	1380
gggtgaggat	ggttctcccc	aagcccatcg	tagaggcccc	acaggctacc	tggtcctgga	1440
tgaggaacag	caaccttcac	agccgcagtc	ggccctggag	tgccaccccc	agagagggtg	1500
cgtcccagag	cctggagccg	ccgtggccgc	cagcaagggg	ctgccgcagc	agctgccagc	1560
acctccggac	gaggatgact	cagctgcccc	atccacgttg	tccctgctgg	gccccacttt	1620
ccccggctta	agcagctgct	ccgctgacct	taaagacatc	ctgagcgagg	ccagcaccat	1680
gcaactcctt	cagcaacagc	agcaggaagc	agtatccgaa	ggcagcagca	gcgggagagc	1740
gagggaggcc	tcggggggctc	ccacttcctc	caaggacaat	tacttagggg	gcacttcgac	1800
catttctgac	aacgccaaag	agttgtgtaa	ggcagtgctg	gtgtccatgg	gcctgggtgt	1860
ggaggcggtt	gagcatctga	gtccaggsga	acagcttcgg	ggggattgca	tgtacgcccc	1920
acttttgagg	gttccacccg	ctgtgcgtcc	cactccttgt	gccccattgg	ccgaatgcaa	1980
aggttctctg	ctagacgaca	gcgcaggcaa	gagcactgaa	gatactgctg	agtattcccc	2040
tttcaaggga	ggttacacca	aagggtctaga	aggcgagagc	ctaggctgct	ctggcagcgc	2100
tgcagcaggg	agctccggga	cacttgaact	gccgtctacc	ctgtctctct	acaagtccgg	2160
agcaactggac	gaggcagctg	cgtaccagag	tcgcgactac	tacaactttc	cactggctct	2220
ggccggaccg	ccgccccctc	cgccgcctcc	ccatccccac	gctcgcatac	agctggagaa	2280
cccgttgga	tacggcagcg	cctggggcgg	tcggcgccgc	cagtgcgcgt	atggggacct	2340
ggcgagcctg	catggcgccg	gtgcagcggg	acccggttct	gggtcaccct	cagccgcgc	2400
ttcctcatcc	tggaacactc	tcttcacagc	cgaagaaggc	cagttgtatg	gaccgtgtgg	2460
tggtggtggg	ggtggtggcg	gcggcgccgg	cggcgccggc	ggcgccggcg	gcggcgccgg	2520
cggcgccggc	gaggcgggag	ctgtagcccc	ctacggctac	actcgccccc	ctcaggggct	2580
ggcgggccag	gaaagcgact	tcaccgcacc	tgatgtgtgg	taccctggcg	gcatggtgag	2640
cagagtggcc	tatccagctc	ccacttgtgt	caaaagcgaa	atggggccct	ggatggatag	2700
ctactccgga	ccttacgggg	acatgcgttt	ggagactgcc	agggaccatg	ttttgcccc	2760
tgactattac	tttccacccc	agaagacctg	cctgatctgt	ggagatgaag	cttctgggtg	2820
tcactattga	gctctcacat	gtggaagctg	caaggtcttc	ttcaaaagag	ccgtgaag	2880
gaaacagaag	tacctgtgcg	ccagcagaaa	tgattgcact	attgataaat	tccgaaggaa	2940
aaattgtcca	tcttgtcgtc	ttcggaatg	ttatgaagca	gggatgactc	tgggagcccc	3000
gaagctgaag	aaacttggtg	atctgaaact	acaggaggaa	ggagaggctt	ccagcaccac	3060
cagccccact	gaggagacaa	cccagaagct	gacagtgtca	cacattgaag	gctatgaatg	3120
tcagcccata	tttctgaatg	tcctggaagc	cattgagcca	ggtgtagtgt	gtgctggaca	3180
cgacaacaac	cagcccgact	cctttgcagc	cttgctctct	agcctcaatg	aactgggaga	3240
gagacagctt	gtacacgtgg	tcaagtgggc	caaggccttg	cctggcttcc	gcaacttaca	3300
cgtggacgac	cagatggctg	tcattcagta	ctcctggatg	gggctcatgg	tgtttgccat	3360
gggctggcga	tccttcacca	atgtcaactc	caggatgctc	tacttgcgcc	ctgatctggg	3420
tttcaatgag	taccgcagtc	acaagtcccg	gatgtacagc	cagtgtgtcc	gaatgaggca	3480
cctctctcaa	gagtttggtg	ggctccaaat	cacccccag	gaattcctgt	gcatgaaagc	3540
actgctactc	ttcagcatta	ttccagtggg	tgggctgaaa	aatcaaaaat	tctttgatga	3600
acttcgaatg	aactacatca	aggaactcga	tcgtatcatt	gcatgcaaaa	gaaaaaatcc	3660
cacatcctgc	tcaagacgct	tctaccagct	caccaagctc	ctggactccg	tgcagcctat	3720
tgcgagagag	ctgcatcagt	tcacttttga	cctgctaate	aagtacacaca	tggtgagcgt	3780
ggactttccg	gaaatgatgg	cagagatcat	ctctgtgcaa	gtgcccaga	tcctttctgg	3840
gaaagtcaag	cccatctatt	tcacacacca	gtgaagcatt	ggaaacccta	tttccccacc	3900
ccagctcatg	ccccctttca	gatgtcttct	gcctgttata	actctgcact	actcctctgc	3960
agtgccctgg	ggaatttgcct	ctattgatgt	acagtctgtc	atgaacatgt	tcctgaattc	4020
tatttgctgg	gctttttttt	tctctttctc	tcctttcttt	ttcttcttcc	ctccctatct	4080
aaccctccca	tggaaccttc	agaactttgt	tcccattgtg	gctcctatct	gtgttttgaa	4140
tggtgttgta	tgccctttaa	tctgtgatga	tcctcatatg	gccagtgctc	aagttgtgct	4200
tgtttacagc	actactctgt	gccagccaca	caaacgttta	cttatcttat	gccacgggaa	4260
gttttagagag	ctaagattat	ctgggggaaat	caaaaacaaa	aacaagcaaa	caaaaaaaaa	4320
a						4321

<210> 5

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

```

Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro
 1          5          10          15
Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys
          20          25          30
Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro
 35          40          45
Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn
 50          55          60
Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu
 65          70          75          80
Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg
          85          90          95
Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu
 100          105          110
Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu
 115          120          125
Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg
 130          135          140
His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu
 145          150          155          160
Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly
          165          170          175
Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Asp
 180          185          190
Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val
 195          200          205
Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala
 210          215          220
Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val
 225          230          235          240
Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Leu Gly Gln Pro Ile
          245          250          255
Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val
 260          265          270
Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr
 275          280          285
Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Asp
 290          295          300
Ser Ser Gly Thr Gly His Phe Thr Ser Gly Val Arg Val Phe Arg Pro
 305          310          315          320
Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr
          325          330          335
Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe
 340          345          350
Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp
 355          360          365
Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro
 370          375          380
Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala
 385          390          395          400
Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala Asn Thr Gly
          405          410          415
Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser
          420          425          430
Thr

```

<210> 6

<211> 1639

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

atcatctata	tgttaaatat	ccgtgccgat	ctgtcttgaa	ggagaaatat	atcgcttggt	60
ttgtttttta	tagtatataa	aaggagtga	aagccaagag	gacgaagtct	ttttcttttt	120
cttctgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaagaca	180
aaaggaagaa	aaggaggaag	gaaggaagaa	gtgattcgcg	aagagagtga	tcatgtcagg	240
gcggcccgag	accacctcct	ttgcggagag	ctgcaagccg	gtgcagcagc	cttcagcttt	300
tggcagcatg	aaagttagca	gagacaagga	cggcagcaag	gtgacaacag	tgggtggcaac	360
tcctgggcag	ggtccagaca	ggccacaaga	agtcagctat	acagacacta	aagtgattgg	420
aaatggatca	tttgggtgtg	tatatcaagc	caaactttgt	gattcaggag	aactggctcg	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcatgagaaa	540
gctagatcac	tgtaacatag	tccgattgcg	ttatttcttc	tactccagtg	gtgagaagaa	600
agatgaggtc	tatcttaatc	tgggtgctga	ctatgttccg	gaaacagtat	acagagttgc	660
cagacactat	agtcgagcca	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatatgta	720
tcagctgttc	cgaagtttag	cctatatcca	ttcctttgga	atctgccatc	gggatattaa	780
accgcagaac	ctcttggttg	atcctgatac	tgctgtatta	aaactctgtg	actttggaag	840
tgcaaaagcag	ctgggtccgag	gagaacccaa	tgtttcgtat	atctgttctc	ggtactatag	900
ggcaccagag	ttgatctttg	gagccactga	ttataacctc	agtatagatg	tatgggtctgc	960
tggctgtgtg	ttggctgagc	tgttactagg	acaaccaata	tttccagggg	atagtgggtg	1020
ggatcagttg	gtagaaataa	tcaaggctct	gggaactcca	acaagggagc	aatcagaga	1080
aatgaaccca	aactacacag	aatttaaatt	ccctcaaatt	aaggcacatc	cttggactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaactcc	1200
accggaggca	attgcactgt	gtagccgtct	gctggagtat	acaccaactg	cccgactaac	1260
accactggaa	gcttgtgcac	attcattttt	tgatgaatta	cgggacccaa	atgtcaaact	1320
accaaatggg	cgagacacac	ctgcactctt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tcacacctctg	gctaccatcc	ttattcctcc	tcattgctcg	attcaagcag	ctgcttcaac	1440
cccacaaaat	gccacagcag	cgtcagatgc	taatactgga	gaccgtggac	agaccaataa	1500
tgctgcttct	gcattcagct	ccaactccac	ctgaacagtc	ccgagcagcc	agctgcacag	1560
gaaaaaacac	cagttacttg	agtgtcactc	agcaacactg	gtcacgtttg	gaaagaatat	1620
taaaaaaaaa	aaaaaaaaaa					1639

<210> 7

<211> 391

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

Met	Lys	Cys	Leu	Val	Thr	Gly	Gly	Asn	Val	Lys	Val	Leu	Gly	Lys	Ala
1				5				10						15	
Val	His	Ser	Leu	Ser	Arg	Ile	Gly	Asp	Glu	Leu	Tyr	Leu	Glu	Pro	Leu
			20					25					30		
Glu	Asp	Gly	Leu	Ser	Leu	Arg	Thr	Val	Asn	Ser	Ser	Arg	Ser	Ala	Tyr
		35				40					45				
Ala	Cys	Phe	Leu	Phe	Ala	Pro	Leu	Phe	Phe	Gln	Gln	Tyr	Gln	Ala	Ala
	50					55				60					
Thr	Pro	Gly	Gln	Asp	Leu	Leu	Arg	Cys	Lys	Ile	Leu	Met	Lys	Ser	Phe
65					70					75					80


```

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
      85      90      95
Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
      100     105     110
His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
      115     120     125
Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
      130     135     140
Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
      145     150     155
Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Arg Val
      165     170     175
Ile Leu Arg Ser Tyr His Glu Glu Glu Ala Asp Ser Thr Ala Lys Ala
      180     185     190
Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
      195     200     205
Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
      210     215     220
Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
      225     230     235
Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
      245     250     255
Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
      260     265     270
Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
      275     280     285
Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
      290     295     300
Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
      305     310     315
Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
      325     330     335
Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
      340     345     350
Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
      355     360     365
Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
      370     375     380
Glu Asp Ser Glu Gly Glu Gly
      385     390

```

<210> 8

<211> 2102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

```

gcgcggaag ggaccccgga cccggaggtc gcggagagct gggcagtgtt ggccgctggc      60
ggagcgctgg ggcagcatga agtgcctggt cacgggcggc aacgtgaagg tgctcggcaa      120
ggccgtccac tccctgtccc gcatcgggga cgagctctac ctggaaccct tggaggacgg      180
gctctccctc cggacggtga actcctcccg ctctgcctat gctgtcttct tctttgcccc      240
gctcttcttc cagcaatacc aggcagccac ccctggtcag gacctgctgc gctgtaagat      300
cctgatgaag tctttcctgt ctgtcttcgg ctcaactggc atgctggaga agacggtgga      360
aaaatgctgc atctccctga atggccggag cagccgcctg gtggtccagc tgcattgcaa      420
gttcgggggtg cggaagactc acaacctgtc cttccaggac tgtgagtccc tgcaggccgt      480
cttcgaccca gctcgtgcc cccacatgct ccgcgccccca gcacgggttc tgggggaggg      540
tgttctgccc ttctctcctg cactggctga agtgacgctg ggcattggcc gtggccgcag      600

```

```

ggtcacccctg cgcagctacc acgaggagga ggcagacagc actgccaaaag ccatgggtgac 660
tgagatgtgc cttgggagagg aggattttcca gcagctgcag gccaggaag ggggtggccat 720
cactttctgc ctcaaggaat tccggggggt cctgagcttt gcagagtcag caaacttgaa 780
tcttagcatt cattttgatg ctccaggcag gcccgccatc ttcacatca aggactcttt 840
gctggacggc cactttgtct tggccacact ctcagacacc gactcgcaact cccaggacct 900
gggctcccca gagcgtcacc agccagtgcc tcagctccag gctcacagca caccaccacc 960
ggacgacttt gccaatgacg acattgactc ttacatgac gccatggaaa ccactatagg 1020
caatgagggc tcgcggtgct tgccctccat ttccttttca cctggccccc agccccccaa 1080
gagccccggc cccactccg aggaggaaga tgaggctgag ccagtagac tgccctgggac 1140
tccccacccc aagaagttcc gctcactgtt cttcggtcc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagtgc ggtgaaggct gaaccaagaa 1260
cctgaagcct gtaccagag gccttgact agacgaagcc ccagccagtgc gcagaactgg 1320
gtctctcagc cctggggatc agaaagggtg gcttgctgga gctgagctgt ttcactgcct 1380
ctgcagggc ccagctggct gtcactgtaa agctgtccca cagcggtcgg gcctgggccc 1440
ttatctcccc acaaccccca gccaatcagg actttccaga cttggccctg aactactgac 1500
gttctacact cttattttctc attgagcctc aggctatact ccagctggcc aaggctggaa 1560
acctgtctcc ctccaggtca ccttcctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gcttctctgc caatcatgac ctgttccttc ctgaagtcct gggcatgcat 1680
ctgggaacccc cgtggagctg acaagttttc cttgctttcc tgatactctt tggcgctgac 1740
ttggaattot aagagccttg gaccggagtg tgtggctagg gttgccctgg ctggggcccc 1800
gtgccgagac tcccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttatc aagagaccag atgggttgcc 1920
ccagatccc gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg caggtgcagg 2040
caggaagcag ccctggggga ctggacgctg ctattgattc attaaaaaa gaaaagaaaa 2100
at 2102

```

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 9
 gggccccctgg atggatagct ac 22

<210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 10
 gtagctatcc atccaggggc c 21

<210> 11
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 11

gggcccctgg atggatagct acctcgaggt agctatccat ccaggggcc

49

<210> 12

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

tttttggggc cctggatgga tagctacctc gaggtagcta tccatccagg ggcc

54

<210> 13

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

Met	Ala	Thr	Ile	Glu	Glu	Ile	Ala	His	Gln	Ile	Ile	Glu	Gln	Gln	Met
1				5					10					15	
Gly	Glu	Ile	Val	Thr	Glu	Gln	Gln	Thr	Gly	Gln	Lys	Ile	Gln	Ile	Val
			20					25					30		
Thr	Ala	Leu	Asp	His	Asn	Thr	Gln	Gly	Lys	Gln	Phe	Ile	Leu	Thr	Asn
		35					40					45			
His	Asp	Gly	Ser	Thr	Pro	Ser	Lys	Val	Ile	Leu	Ala	Arg	Gln	Asp	Ser
	50					55					60				
Thr	Pro	Gly	Lys	Val	Phe	Leu	Thr	Thr	Pro	Asp	Ala	Ala	Gly	Val	Asn
65					70					75				80	
Gln	Leu	Phe	Phe	Thr	Thr	Pro	Asp	Leu	Ser	Ala	Gln	His	Leu	Gln	Leu
				85				90					95		
Leu	Thr	Asp	Asn	Ser	Pro	Asp	Gln	Gly	Pro	Asn	Lys	Val	Phe	Asp	Leu
			100					105					110		
Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Arg	His	Tyr	Gly	Ala	Val
		115					120				125				
Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Ser	Ile	Arg	Lys	Asn
	130					135					140				
Leu	Val	Tyr	Ser	Cys	Arg	Gly	Ser	Lys	Asp	Cys	Ile	Ile	Asn	Lys	His
145					150					155				160	
His	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu	Gln	Arg	Cys	Ile	Ala	Phe
			165					170					175		
Gly	Met	Lys	Gln	Asp	Ser	Val	Gln	Cys	Glu	Arg	Lys	Pro	Ile	Glu	Val
			180					185					190		
Ser	Arg	Glu	Lys	Ser	Ser	Asn	Cys	Ala	Ala	Ser	Thr	Glu	Lys	Ile	Tyr
		195				200						205			
Ile	Arg	Lys	Asp	Leu	Arg	Ser	Pro	Leu	Thr	Ala	Thr	Pro	Thr	Phe	Val
	210					215					220				
Thr	Asp	Ser	Glu	Ser	Thr	Arg	Ser	Thr	Gly	Leu	Leu	Asp	Ser	Gly	Met
225					230					235				240	
Phe	Met	Asn	Ile	His	Pro	Ser	Gly	Val	Lys	Thr	Glu	Ser	Ala	Val	Leu
			245						250					255	
Met	Thr	Ser	Asp	Lys	Ala	Glu	Ser	Cys	Gln	Gly	Asp	Leu	Ser	Thr	Leu
		260						265					270		
Ala	Asn	Val	Val	Thr	Ser	Leu	Ala	Asn	Leu	Gly	Lys	Thr	Lys	Asp	Leu
		275					280						285		

```

Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
 290          295          300
Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
305          310          315          320
Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
          325          330          335
Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
          340          345          350
Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
          355          360          365
Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
          370          375          380
Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
385          390          395          400
Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
          405          410          415
Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
          420          425          430
Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
          435          440          445
Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
          450          455          460
Asp Ala Lys Val Ile Ala Ala Leu Ile His Phe Thr Arg Arg Ala Ile
465          470          475          480
Thr Asp Leu

```

<210> 14

<211> 596

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

```

Met Thr Ser Pro Ser Pro Arg Ile Gln Ile Ile Ser Thr Asp Ser Ala
 1          5          10          15
Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
          20          25          30
Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
          35          40          45
Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
          50          55          60
Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
65          70          75          80
Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
          85          90          95
Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
          100          105          110
Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
          115          120          125
Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
          130          135          140
Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
145          150          155          160
Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
          165          170          175
Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
          180          185          190

```

```

Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
    195                200                205
Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
    210                215                220
Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
    225                230                235                240
Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
    245                250                255
Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
    260                265                270
Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
    275                280                285
Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
    290                295                300
Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
    305                310                315                320
Asn Thr Thr Asp Ser Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
    325                330                335
Thr Ser Gly Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
    340                345                350
Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
    355                360                365
Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
    370                375                380
Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
    385                390                395                400
Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
    405                410                415
Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
    420                425                430
Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
    435                440                445
Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
    450                455                460
Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
    465                470                475                480
Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
    485                490                495
Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
    500                505                510
Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
    515                520                525
Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
    530                535                540
Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
    545                550                555                560
Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
    565                570                575
Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
    580                585                590
Gly Ala Ser Leu
    595

```

<210> 15

<211> 2029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

gaattcgggc	ccgtcggctt	tcttcaaccc	tctcttcccg	gagcgcgcc	aatccacgag	60
tgccagccgc	gggactgtcg	cgtcggcgcc	cgacgcggag	tcagcagggg	cgaaaagcgg	120
tagatcatgg	caaccataga	agaaattgca	catcaaatta	ttgaacaaca	gatgggagag	180
attgttacag	agcagcaaac	tgggcagaaa	atccagattg	tgacagcact	tgatcataat	240
acccaaggca	agcagttcat	tctgacaaat	cacgacggct	ctactccaag	caaagtcatt	300
ctggccaggc	aagattccac	tccgggaaaa	gttttcccta	caactccaga	tgcagcaggt	360
gtcaaccagt	tatttttttac	cactcctgat	ctgtctgcac	aacacctgca	gctcctaaca	420
gataattctc	cagaccaagg	accaaataag	gttttttgatc	tttgcgtagt	atgtggagac	480
aaagcatcag	gacgtcatta	tgagagcagta	acttgtgaag	gctgcaaagg	atTTTTTaaa	540
agaagcatcc	gaaaaaattt	agtatatcca	tgtcgaggat	caaaggattg	tattattaat	600
aagcaccacc	gaaaccgctg	tcaatactgc	agggttacaga	gatgtattgc	gtttggaatg	660
aagcaagact	ctgtccaatg	tgaaagaaaa	cccatgaag	tatcacgaga	aaaatcttcc	720
aactgtgccg	cttcaacaga	aaaaatctat	atccgaaagg	accttcgtag	cccatctaact	780
gcaactccaa	cttttgtaac	agatagtga	agtacaaggt	caacaggact	gttagattca	840
ggaatgttca	tgaatatcca	tccatctgga	gtaaaaactg	agtcagctgt	gctgatgaca	900
tcagataagg	ctgaatcatg	tcaggagat	ttaagtacat	tgcccaatgt	ggttacatca	960
ttagcgaatc	ttggaaaaaac	ttaaagatctt	tctcaaaata	gtaatgaaa	gtctatgatt	1020
gaaagcttaa	gcaatgatga	tacctctttg	tgtgaatttc	aagaaatgca	gaccaacggg	1080
gatgtttcaa	gggcatttga	cactcttgca	aaagcattga	atcctggaga	gagcacagcc	1140
tgccagagct	cagtagcggg	catggaagga	agtgtaacac	taatcactgg	agattcaagc	1200
ataaattaca	ccgaaaaaga	ggggccactt	ctcagcgatt	cacatgtagc	tttcaggctc	1260
accatgcctt	ctcctatgcc	tgagtacctg	aatgtgcact	acattgggga	gtctgcctcc	1320
agactgctgt	tcttatcaat	gcactgggca	ctttcgattc	cttctttcca	ggctctaggg	1380
caagaaaaca	gcatatcact	ggtgaaagct	tactggaatg	aactttttac	tcttggtctt	1440
gcccagtgct	ggcaagtgat	gaatgtagca	actatattag	caacatttgt	caattgtctt	1500
cacaatagtc	ttcaacaaga	tgccaaggta	attgcagccc	tcattcattt	cacaagacga	1560
gcaatcactg	atTTTataaat	gcttaactat	agaatggctt	atgactaccc	aaaacagtgc	1620
cccatcaaca	aatggggaaa	attgcctttt	gagctcagga	ataatttata	aattggggac	1680
taccttttag	ttcttttagca	tattctattt	cttattgttt	tataataatt	ttaaatcatt	1740
tgcttcctcc	ttatgtttta	cagcagaggg	gtaatcacct	taaaatgtca	tcaaaaatag	1800
atctactaga	aggcagcatc	acattcccat	cttacttatg	gactcctacc	cctgggttcac	1860
gtcttatatg	cctgtaaatg	ttataaagcc	taccttcagg	aaagctatgg	ttgactaatt	1920
actaatggat	gggtttttaa	catgtccctc	tacaataaat	taaaatcttt	caatgtttga	1980
atataatgtg	gaggtgttta	cctgagggcc	tctctatctc	cccgaattc		2029

<210> 16

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

gagttgtgcc	tgagtgatg	tttaagccaa	tgtcagggca	aggcaacagt	ccctggccgt	60
cctccagcac	ctttgtaatg	catatgagct	cgggagacca	gtacttaaag	ttggaggccc	120
gggagcccag	gagctggcgg	agggcggtcg	tcctgggagc	tgacttgct	ccgtcgggtc	180
gccggcttca	ccggaccgca	ggctcccggg	gcagggccgg	ggccagagct	cgctgtctgg	240
cgggacatgc	gctgcgtcgc	ctctaaccctc	gggctgtgct	ctttttccag	gtggcccgcg	300
ggtttctgag	ccttctgccc	tgcggggaca	cggctctgcac	cctgcccgcg	gccacggacc	360
atgaccatga	ccctccacac	caaagcatct	gggatggccc	tactgcatca	gatccaaggg	420
aacgagctgg	agccccgtga	ccgtccgcag	ctcaagatcc	ccctggagcg	gccccctggg	480
gaggtgtacc	tggaacagcag	caagcccgcg	gtgtacaact	accccagagg	cgccgcctac	540
gagttcaacg	ccgcgggcgc	cgccaacgcg	caggtctacg	gtcagaccgg	cctcccctac	600
ggccccgggt	ctgaggtctgc	ggcggttcgcg	tccaacggcc	tggggggttt	ccccccactc	660
aacagcgtgt	ctccgagccc	gctgatgcta	ctgcacccgc	cgccgcagct	gtcgcccttc	720
ctgcagcccc	acggccagca	ggtgccctac	tacctggaga	acgagcccag	cggctacacg	780
gtgcgcgagg	ccggcccgcg	ggcattctac	aggccaaatt	cagataatcg	acgccagggt	840

ggcagagaaa	gattggccag	taccaatgac	aagggaagta	tggctatgga	atctgccaaag	900
gagactcgct	actgtgcagt	gtgcaatgac	tatgcttcag	gctaccatta	tggagtcttg	960
tcctgtgagg	gctgcaaggc	cttcttcaag	agaagtattc	aaggacataa	cgactatatg	1020
tgtccagcca	ccaaccagtg	caccattgat	aaaaaacagga	ggaagagctg	ccaggcctgc	1080
cggctccgca	aatgctacga	agtgggaatg	atgaaagggtg	ggatacgaaa	agaccgaaga	1140
ggagggagaa	tgttgaaaca	caagcgccag	agagatgatg	gggagggcag	gggtgaagtg	1200
gggtctgctg	gagacatgag	agctgccaac	ctttggccaa	gcccgcctcat	gatcaaacgc	1260
tctaagaaga	acagcctggc	cttgtccctg	acggccgacc	agatgggtcag	tgccttggtg	1320
gatgctgagc	ccccatact	ctattccgag	tatgatccta	ccagaccctt	cagtgaagct	1380
tcgatgatgg	gcttactgac	caacctggca	gacagggagc	tggttcacat	gatcaactgg	1440
gcgaagaggg	tgccaggctt	tgtggatttg	accctccatg	atcaggtcca	ccttctagaa	1500
tgtgcctggc	tagagatcct	gatgattggg	ctcgtctggc	gctccatgga	gcaccagtg	1560
aagctactgt	ttgctcctaa	cttgcctctg	gacaggaacc	agggaaaatg	tgtagagggc	1620
atgggtggaga	tcttcgacat	gctgctggct	acatcatctc	ggttccgcat	gatgaatctg	1680
cagggagagg	agtttgtgtg	cctcaaactc	attattttgc	ttaattcttg	agtgtacaca	1740
tttctgtcca	gcaccctgaa	gtctctggaa	gagaaggacc	atatccaccg	agtcctggac	1800
aagatcacag	acactttgat	ccacctgatg	gccaaaggcag	gcctgaccct	gcagcagcag	1860
caccagcggc	tggcccagct	cctcctcatc	ctctcccaca	tcaggcacat	gagtaacaaa	1920
ggcatggagc	atctgtacag	catgaagtgc	aagaacgtgg	tgcccctcta	tgacctgctg	1980
ctggagatgc	tggacgcccc	cgcctacat	gcgcccacta	gccgtggagg	ggcatccgtg	2040
gaggagacgg	accaagcca	cttggccact	gcgggctcta	cttcacgcga	ttccttgcaa	2100
aagtattaca	tcacggggga	ggcagagggg	ttccctgcca	cagtctgaga	gctccctggc	2160
tcccacacgg	ttcagataat	cctgctgca	ttttaccctc	atcatgcacc	acttttagcca	2220
aattctgtct	cctgcataca	ctccggcatg	catccaacac	caatggcttt	ctagatgagt	2280
ggccattcat	ttgcttgctc	agttcttagt	ggcacatctt	ctgtcttctg	ttgggaacag	2340
ccaaagggat	tccaaggcta	aatccttgta	acagctctct	ttcccccttg	ctatgttact	2400
aagcgtgagg	attcccgtag	ctcttcacag	ctgaactcag	tctatgggtt	ggggctcaga	2460
taactctgtg	catttaagct	actttagtag	accaggcct	ggagagtaga	cattttgcct	2520
ctgataagca	cttttttaaat	ggctctaaga	ataagccaca	gcaaagaatt	taaagtggct	2580
cctttaattg	gtgacttgga	gaaagctagg	tcaaggggtt	attatagcac	cctcttgbat	2640
tcctatggca	atgcactcct	ttatgaaagt	ggtaacacct	aaagctttta	tatgactgta	2700
gcagagtatc	tgggtgattgt	caattcactt	ccccttatag	gaatacaagg	ggccacacag	2760
ggaaggcaga	tcccctagtt	ggccaagact	tatttttaact	tgatacactg	cagattcaga	2820
gtgtcctgaa	gctctgcctc	tggctttccg	gtcatgggtt	ccagttaatt	catgcctccc	2880
atggacctat	ggagagcaac	aagttgatct	tagttaagtc	tccctatatg	agggataagt	2940
tcctgatattt	tgtttttatt	tttgtgttac	aaaagaaagc	cctccctccc	tgaacttgca	3000
gtaagggtcag	cttcaggacc	tgttccagtg	ggcactgtac	ttggatcttc	ccggcgtgtg	3060
tgtgccttac	acaggggtga	actgttcact	gtgggtgatg	atgatgaggg	taaatggtag	3120
ttgaaaggag	cagggggccct	ggtgttgcat	ttagccctgc	ggcatggagc	tgaacagtac	3180
ttgtgcagga	ttgttgtggc	tactagagaa	caagagggaa	agtagggcag	aaactgggata	3240
cagttctgag	cacagccaga	cttgcctcagg	tggccctgca	caggctgcag	ctacctagga	3300
acattccttg	cagaccccg	attgcctttg	ggggtgcctt	gggatccctg	gggtagtcca	3360
gctcttattc	atttcccagc	gtggccctgg	ttggaagaag	cagctgtcaa	gttgtagaca	3420
gctgtgttcc	tacaattggc	ccagcaccct	ggggcacggg	agaaggggtg	ggaccgttgc	3480
tgtcactact	caggctgact	ggggcctggg	cagattacgt	atgcccttgg	tggtttagag	3540
ataatccaaa	atcagggttt	ggtttgggga	agaaaatcct	cccccttcc	ccccgcgcc	3600
gttccctacc	gcctccactc	ctgccagctc	atttcccttc	atttcccttg	acctataggg	3660
taaaaaagaa	aggctcattc	cagccacagg	gcagccctcc	ctgggccttt	gcttctctag	3720
cacaattatg	ggttactctc	tttttcttaa	caaaaaagaa	tgtttgattt	cctctgggtg	3780
accttattgt	ctgtaattga	aaccctattg	agaggtgatg	tctgtgttag	ccaatgacct	3840
aggtagctgc	tgggcttct	cttgggtatg	cttgttttga	aaagtggatt	tcattcattt	3900
ctgattgtcc	agttaagtga	tcaccaaagg	actgagaatc	tgggagggca	aaaaaaaaaa	3960
aaaaagtttt	tatgtgcact	taaatttggg	gacaatttta	tgtatctgtg	tttaaggatat	4020
gcttaagaac	ataattcttt	tgttgctgtt	tgtttaagaa	gcaccttagt	ttgtttaaga	4080
agcaccttat	atagtataat	atatattttt	ttgaaattac	attgcttgtt	tatcagacaa	4140
ttgaatgtag	taattctggt	ctggatttaa	tttgactggg	ttaacatgca	aaaaccaagg	4200
aaaaatatatt	agtttttttt	tttttttttg	tatacttttc	aagctacctt	gtcatgtata	4260
cagtcattta	tgccataaagc	ctgggtgatta	ttcattttaaa	tgaagatcac	atttcatatc	4320
aactttttgta	tccacagtag	acaaaatagc	actaatccag	atgcctattg	ttggatatattg	4380
aatgacagac	aatcttatgt	agcaaagatt	atgcctgaaa	aggaaaatta	ttcagggcag	4440
ctaatttttgc	ttttacccaa	atatcagtag	taatattttt	ggacagtagc	taatgggtca	4500

```

gtggggttctt tttaatgttt atacttagat tttcttttaa aaaaattaaa ataaaacaaa 4560
aaaaatttctt aggactagac gatgtaatac cagctaaagc caaacaatta tacagtggaa 4620
gggttttacat tattcatcca atgtgtttct attcatgtta agatactact acatttgaag 4680
tgggcagaga acatcagatg attgaaatgt tcgcccaggg gtctccagca actttggaaa 4740
tctctttgta tttttacttg aagtggccact aatggacagc agatattttc tggctgatgt 4800
tggtattggg tgtaggaaca tgatttaaaa aaaaaactct tgcctctgct tccccccact 4860
ctgaggcaag ttaaaatgta aaagatgtga tttatctggg gggctcaggt atgggtgggga 4920
agtggattca ggaatctggg gaatggcaaa tatattaaga agagtattga aagtatttgg 4980
aggaaaatgg ttaattctgg gtgtgcacca aggttcagta gagtccactt ctgccctgga 5040
gaccacaaat caactagctc catttacagc catttctaaa atggcagctt cagttctaga 5100
gaagaaagaa caacatcagc agtaaagtcc atggaatagc tagtggctctg tgtttctttt 5160
cgccattgcc tagcttgccg taatgattct ataatgccat catgcagcaa ttatgagagg 5220
ctaggtcatc caaagagaag accctatcaa tgtagggtgc aaaatctaac ccctaaggaa 5280
gtgcagctct tgatttgatt tccctagtaa ccttgccagat atgtttaacc aagccatagc 5340
ccatgccttt tgagggtctga acaaataagg gacttactga taatttactt ttgatcacat 5400
taagggtgtt tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc 5460
ttagagtact ccttccccctg catgacactg attacaaata ctttcctatt catactttcc 5520
aattatgaga tggactgtgg gtactgggag tgatcactaa caccatagta atgtctaata 5580
ttcacaggca gatctgcttg gggaagctag ttaatgtgaaa ggcaaataaa gtcatacagt 5640
agctcaaaaag gcaaccataa ttctcttttg tgcaagtctt gggagcgtga tctagattac 5700
actgcaccat tcccaggtta atcccctgaa aacttactct caactggagc aaatgaactt 5760
tgggtcccaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc 5820
ctttccaaat gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
attgctgcct ctattatggc acttcaattt tgcactgtct tttgagattc aagaaaaatt 5940
tctattcatt tttttgcac caattgtgcc tgaactttta aaatatgtaa atgctgccat 6000
gttccaaacc catogtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt 6060
gtcccatgag cagggtgcctg agacacagac ccctttgcat tcacagagag gtcattgggt 6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa 6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaagtcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact 6300
gatgtgactc ggttttgcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgactttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacia ttttctcaac 6420
ctatttgatg ttcaaataaa gaattaaact

```

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

cgctgtaaga tctgatgaa gtc

23

<210> 18

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

tgctctctcc tcgtggtag

19

<210> 19

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19
 tgccttcctt ggatgtggta g 21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
 cgtctgccct atcaactttc g 21

<210> 21
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 21
 Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1 5 10 15
 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30
 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220

Tyr	Leu	Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala	Lys	Glu	Leu	Cys
225					230					235					240
Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His
				245					250					255	
Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu
			260					265					270		
Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala
		275					280					285			
Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu
	290					295					300				
Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu
305					310					315					320
Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser
				325				330						335	
Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala
			340					345						350	
Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro
	355						360						365		
Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His
	370					375						380			
Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala
385					390					395					400
Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly
				405					410					415	
Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser
			420					425					430		
Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly
	435						440					445			
Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	450					455					460				
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro
465					470					475					480
Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp
				485					490					495	
Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val
			500					505					510		
Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met
	515						520					525			
Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg
	530					535					540				
Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys
545					550					555					560
Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr
				565					570					575	
Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln
			580					585					590		
Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	His
		595					600					605			
Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly
	610					615					620				
Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu
625					630					635					640
Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr
				645					650					655	
Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro
			660					665					670		
Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala
			675				680					685			
Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser
	690					695						700			

Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala
 705 710 715 720
 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
 805 810 815
 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
 885 890 895
 Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
 900 905 910
 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

<210> 22

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22

 Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser Ile
 1 5 10

<210> 23

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23

 His Pro Thr His Ser Ser Arg Leu Trp Glu Leu Leu Met Glu Ala Thr
 1 5 10 15
 Pro Thr Met